



SEQUENCE LISTING

per
#19

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NAKAYAMA, Toru

<120> GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130> 001560-377

<140> US 09/446,089

<141> 1999-12-17

<150> PCT/JP99/02045

<151> 1999-04-16

<150> JP 10/107296

<151> 1998-04-17

<160> 15

<170> PatentIn version 3.0

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<211> 1951

<212> DNA

<213> Antirrhinum majus

<220>

<221> CDS

<222> (96)..(1781)

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Met Phe Lys Asn Pro Asn
1 5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Gln Glu
10 15 20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
25 30 35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
40 45 50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
55 60 65 70

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tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt	353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys	
75 80 85	
ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc	401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser	
90 95 100	
act acc atg agg gtt cgc cgt gct cat tta gtt gat gat gca tac	449
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr	
105 110 115	
att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag	497
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu	
120 125 130	
gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac	545
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr	
135 140 145 150	
tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa	593
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln	
155 160 165	
atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac	641
Ile His Arg Ser Trp Leu Phe Pro Phe His Arg Tyr Tyr Ile Tyr	
170 175 180	
ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct	689
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala	
185 190 195	
ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca	737
Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser	
200 205 210	
atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt	785
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser	
215 220 225 230	
aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat	833
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp	
235 240 245	
tcc gac aat acc act act cct gaa gag oaa atg att ata aac ctt aaa	881
Ser Asp Asn Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys	
250 255 260	
att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc	929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe	
265 270 275	
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Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly	
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Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser	

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aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp 330		335		340
tcc ata tgg aag acc cta gga ggg ccg ccg agg acg gac tta aca gat Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp 345		350		355
cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu 360		365		370
atg gtt cgg gtc aag gtt ccg gat tgc tta gat gaa aag aaa cta ggg Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly 375		380		390
tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr 395		400		405
cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr 410		415		420
gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys 425		430		435
gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp 440		445		450
gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp 455		460		470
cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp 475		480		485
ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val 490		495		500
agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu 505		510		515
tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu 520		525		530

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Asp	Asp	Tyr	Val	Leu	Val	Thr	Leu	Val	Pro	Arg	Asn	Ala	Gly	Asp	Ala	
535				540				545						550		
atc	aag	att	cat	aat	gtc	aag	att	gag	ctt	gat	ggc	taataaaattc			1791	
Ile	Lys	Ile	His	Asn	Val	Lys	Ile	Glu	Ileu	Asp	Gly					
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Phe	Ile	Ile	Thr	Leu	Phe	Leu	Leu	Ile	Val	Gly	Leu	Tyr	Ile	Ala	Asn	
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Ser	Leu	Ala	Tyr	Ala	Arg	Phe	Ala	Ser	Thr	Ser	Thr	Gly	Pro	Ile	Ala	
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Ala	Pro	Asp	Val	Thr	Lys	Cys	Gly	Gln	Pro	Asp	Leu	Pro	Pro	Gly	Thr	
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Ala	Pro	Ile	Asn	Cys	Cys	Pro	Pro	Ile	Pro	Ala	Lys	Ile	Ile	Asp	Phe	
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Glu	Leu	Pro	Pro	Pro	Ser	Thr	Thr	Met	Arg	Val	Arg	Arg	Ala	Ala	His	
				100				105					110			
Leu	Val	Asp	Asp	Ala	Tyr	Ile	Ala	Lys	Phe	Lys	Lys	Ala	Val	Glu	Leu	
				115				120					125			
Met	Arg	Ala	Leu	Pro	Glu	Asp	Asp	Pro	Arg	Ser	Phe	Lys	Gln	Gln	Ala	
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Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
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Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
 165 170 175

His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
 180 185 190

Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
 195 200 205

Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
 210 215 220

Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
 225 230 235 240

Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
 245 250 255

Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
 260 265 270

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
 275 280 285

Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
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His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
 305 310 315 320

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
 325 330 335

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
 340 345 350

Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
 355 360 365

Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
 370 375 380

Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
 385 390 395 400

Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
 405 410 415

Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
 420 425 430

Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
 435 440 445

Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
 450 455 460

Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
 465 470 475 480

Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
 485 490 495

Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
 500 505 510

Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
 515 520 525

Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
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Asp Gly

<210> 3
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 <213> *Antirrhinum majus*

<400> 3

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<210> 4
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<212> PRT
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Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
1 5 10

<210> 5
<211> 18
<212> PRT
<213> *Antirrhinum majus*

<400> 5

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
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Glu Phe

<210> 6
<211> 29
<212> PRT
<213> *Antirrhinum majus*

<220>
<221> UNSURE
<222> (9)..(9)
<223> Amino acid 9 is Xaa wherein Xaa = unknown or other.

<220>
<221> UNSURE
<222> (29)..(29)
<223> Amino acid 29 is Xaa wherein Xaa = unknown or other.

<400> 6

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Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys
20 25

<210> 7
<211> 125
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<213> *Antirrhinum majus*

<400> 7

Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe Phe Gly Arg
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Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly Ser Ile Glu
 20 25 30

Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr
 35 40 45

Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro
 50 55 60

Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp
 65 70 75 80

Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe
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Leu Asp Ala Ser Phe Val Phe Cys Asp Glu Asn Ala Glu Met Val Arg
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Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly
 115 120 125

<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (2)..(2)

<223> Amino acid 2 is Xaa wherein Xaa = Val or Ile.

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Phe Xaa Lys Phe Thr Ala Ile
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<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (6)..(6)

<223> Amino acid 6 is Xaa wherein Xaa = Thr or Pro.

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 1 5

<210> 10

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 10

His Ala Val Cys Asn Glu
1 5

<210> 11
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<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (6)..(18)
<223> Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g or t/u or unknown or other

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<210> 12
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (12)..(12)
<223> Nucleotide 12 is "n" wherein "n" = a or c or g or t/u or unknown or other

<400> 12
aartggaarg gnaarmc 17

<210> 13
<211> 18
<212> DNA
<213> Primer

<220>
<221> misc_feature
<222> (4)..(7)
<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or t/u or unknown or other

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rtgngcnacr carttytc 18

<210> 14
<211> 20
<212> DNA
<213> Primer

<400> 14
aaggatccgg ccctatcgcc 20

<210> 15
<211> 22
<212> DNA
<213> Primer

<400> 15
gggttcgaag aattcatctc tg

22